

What is claimed is:

~~Patent claims~~

1. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence which codes for the luxS gene, chosen from the group consisting of
- 5 a) polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,
- 10 b) polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least 70% to the amino acid sequence of SEQ ID No. 2,
- c) polynucleotide which is complementary to the polynucleotides of a) or b), and
- 15 d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c),
- the polypeptide preferably having the activity of the histidine kinase LuxS.
- 20 2. A polynucleotide as claimed in claim 1, wherein the polynucleotide is a preferably recombinant DNA which is capable of replication in coryneform bacteria.
3. A polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.
- 25 4. A polynucleotide as claimed in claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.
5. A DNA as claimed in claim 2 which is capable of replication, comprising

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- (i) the nucleotide sequence shown in SEQ ID No. 1,  
or
- (ii) at least one sequence which corresponds to  
sequence (i) within the range of the  
degeneration of the genetic code, or
- (iii) at least one sequence which hybridizes with the  
sequence complementary to sequence (i) or (ii),  
and optionally
- (iv) sense mutations of neutral function in (i).
6. A DNA as claimed in claim 2 which is capable of  
replication, wherein the hybridization is carried out  
under a stringency corresponding to at most 2x SSC.
7. A polynucleotide sequence as claimed in claim 1, which  
codes for a polypeptide which comprises the amino acid  
sequences shown in SEQ ID No. 2.
8. A coryneform bacterium in which the luxS gene is  
attenuated, in particular eliminated.
9. The vector pCR2.1luxSint, which
- 9.1 carries an internal fragment of the luxS gene  
492 bp in size,
- 9.2 the restriction map of which is reproduced in  
figure 1, and
- 9.3 which is deposited in the E. coli strain  
Top10/pCR2.1luxSint under no. DSM 14082 at the  
Deutsche Sammlung für Mikroorganismen und  
Zellenkulturen [German Collection of  
Microorganisms and Cell Cultures].

10. A process for the fermentative preparation of L-amino acids, in particular lysine, which comprises carrying out the following steps:
- 5 a) fermentation of the coryneform bacteria which produce the desired L-amino acid and in which at least the luxS gene or nucleotide sequences which code for it are attenuated, in particular eliminated;
  - b) concentration of the L-amino acid in the medium or in the cells of the bacteria, and
  - 10 c) isolation of the L-amino acid.
11. A process as claimed in claim 10, wherein bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.
- 15 12. A process as claimed in claim 10, wherein bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.
- 20 13. A process as claimed in claim 10, wherein the expression of the polynucleotide(s) which code(s) for the luxS gene is attenuated, in particular eliminated.
- 25 14. A process as claimed in claim 10, wherein the regulatory or catalytic properties of the polypeptide (enzyme protein) for which the polynucleotide luxS codes are reduced.
15. A process as claimed in claim 10, wherein for the preparation of L-amino acids, coryneform microorganisms in which at the same time one or more of the genes chosen from the group consisting of
- 30 15.1 the dapA gene which codes for dihydrodipicolinate synthase,

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- 15.2 the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,
- 15.3 the tpi gene which codes for triose phosphate isomerase,
- 5 15.4 the pgk gene which codes for 3-phosphoglycerate kinase,
- 15.5 the zwf gene which codes for glucose 6-phosphate dehydrogenase,
- 10 15.6 the pyc gene which codes for pyruvate carboxylase,
- 15.7 the mqo gene which codes for malate-quinone oxidoreductase,
- 15.8 the lysC gene which codes for a feed-back resistant aspartate kinase,
- 15 15.9 the lysE gene which codes for lysine export,
- 15.10 the hom gene which codes for homoserine dehydrogenase
- 20 15.11 the ilvA gene which codes for threonine dehydratase or the ilvA(Fbr) allele which codes for a feed back resistant threonine dehydratase,
- 15.12 the ilvBN gene which codes for acetohydroxy-acid synthase,
- 25 15.13 the ilvD gene which codes for dihydroxy-acid dehydratase,
- 15.14 the zwal gene which codes for the Zwal protein
- is/are enhanced or over-expressed are fermented.

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16. A process as claimed in claim 10, wherein for the preparation of L-amino acids, coryneform microorganisms in which at the same time one or more of the genes chosen from the group consisting of
- 5 16.1 the pck gene which codes for phosphoenolpyruvate carboxykinase,
- 16.2 the pgi gene which codes for glucose 6-phosphate isomerase,
- 16.3 the poxB gene which codes for pyruvate oxidase
- 10 16.4 the zwa2 gene which codes for the Zwa2 protein is or are attenuated are fermented.
17. A coryneform bacterium which contains a vector which carries parts of the polynucleotide but at least 15 successive nucleotides of the sequence as claimed in claim 1.
- 15 18. A process as claimed in one or more of the preceding claims, wherein microorganisms of the species *Corynebacterium glutamicum* are employed.
19. A process for discovering RNA, cDNA and DNA in order to
- 20 isolate nucleic acids, or polynucleotides or genes which code for the histidine kinase LuxS or have a high similarity with the sequence of the luxS gene, which comprises employing the polynucleotide comprising the polynucleotide sequences as claimed in claims 1, 2, 3
- 25 or 4 as hybridization probes.